We claim:

1. An isolated compound which binds to a pilus subunit groove thereby inhibiting pilus assembly.

2. The compound of claim 1 wherein the compound is a peptide.

3. The compound of claim 1 wherein the compound is a non-peptide compound.

4. The compound of claim 1 further comprising a mimic of a chaperone G_1 beta-strand with at least two alternating hydrophobic amino acid residues which exhibits antibacterial activity against a Gram-negative bacterium.

5. The compound of claim 4 wherein said mimic further comprises the amino acid sequence NVLQIAL (SEQ ID NO: 1) or an analogue thereof.

6. The compound of claim 4 wherein the mimic has been modified to improve binding, specificity, solubility, safety, or efficacy.

7. The mimic of claim 4 wherein said mimic exhibits antibacterial activity against a Gram-negative bacterium comprising *Escherichia coli, Haemophilus influenzae, Salmonella enteriditis, Salmonella typhimurium, Bordetella pertussis, Yersinia pestis, Yersinia enterocolitica, Helicobacter pylori and Klebsiella pneumoniae.*

8. The compound of claim 1 further comprising a mimic of an amino-terminal motif of a pilus subunit with at least two alternating hydrophobic amino acid residues which mimic exhibits antibacterial activity against a Gram-negative bacterium.

9. The compound of claim 8 wherein said mimic of an amino-terminal motif of a pilus subunit further comprises the amino acid sequence SDVAFRGNLL (SEQ ID NO: 12) or an analogue thereof.

10. The compound of claim 9 wherein said mimic has been modified to improve binding, specificity, solubility, safety, or efficacy.

11. The compound of claim 8 wherein said mimic exhibits antibacterial activity against a Gram-negative bacterium comprising *Escherichia coli, Haemophilus influenzae, Salmonella enteriditis, Salmonella typhimurium, Bordetella pertussis, Yersinia pestis, Yersinia enterocolitica, Helicobacter pylori and Klebsiella pneumoniae.*

12. The compound of claim 1 which is a 10 to 20 residue peptide or peptide analog according to formula (I):

SUB A4

(I) Z_1~Z_2–X_1–X_2–X_3–X_4–X_5–X_6–X_7–X_8–X_9–X_{10}–Z_3~Z_4

or a pharmaceutically-acceptable salt thereof, wherein:

Z_1 is R–C(O)–NR– or RRN–;

Z_2 is an optional 1 to 5 residue peptide or peptide analog;

X_1 is any amino acid residue;

X_2 is any amino acid residue;

X_3 is a hydrophobic residue or a hydroxyl-substituted aliphatic residue;

X_4 is any amino acid residue;

X_5 is a hydrophobic residue or Gly;

X_6 is a hydrophobic or a hydrophilic residue;

X_7 is Gly, an amide-substituted polar residue or a hydrophobic residue;

X_8 is any amino acid residue;

X_9 is an aliphatic residue;

X_{10} is any amino acid residue;

Z_3 is an optional 1 to 5 residue peptide or peptide analog;

Z_4 is –C(O)OR or –C(O)NRR;

each R is independently hydrogen, (C_1-C_6) alkyl, (C_2-C_6) alkenyl, (C_2-C_6) alkynyl or (C_6-C_{14}) aryl;

each "–" between residues X_1 through X_{10}, Z_2 and X_1 and X_{10} and Z_3 independently represents an amide linkage, a substituted amide linkage or an isostere of an amide likage; and

each "~" represents a bond

13. The compound of claim 12 wherein said compound further comprises one or more features selected from the group consisting of:

each "–" between residues X_1 through X_{10}, Z_2 and X_1 and X_{10} and Z_3 is an amide linkage;

Z_1 is H_2N–;

Z_4 is –C(O)OH or a salt thereof;

optional Z_2 is not present;

optional Z_3 is not present;

X_1 is other than a basic residue;

X_2 is other than an aliphatic residue;

X_3 is an aliphatic residue or T;

X_4 is other than an acidic residue;

X_5 is an aliphatic residue, F or G;

X_7 is G, N or A;

X_8 is other than an aliphatic residue; and

X_{10} is an aliphatic or a polar residue.

14. The compound of claim 13 which is selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17,

SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

15. The compound of claim 12 wherein said compound exhibits antibacterial activity against a Gram-negative bacterium comprising *E. coli, H. influenzae, S. euteriditis, S. typhimurium, B. pertussis, Y. pestis, Y. entarocolitica, H. pylori and K. pneumoniae.*

16. The antibacterial compound of claim 1 which is a 7 to 17 residue peptide or peptide analog according to formula (II):

(II) Z_{11}~Z_{12}–X_{11}–X_{12}–X_{13}–X_{14}–X_{15}–X_{16}–X_{17}–Z_{13}~Z_{14}

or a pharmaceutically-acceptable salt thereof, wherein:

Z_{11} is R'–C(O)–NR'– or R'R'N–;

Z_{12} is an optional 1 to 5 residue peptide or peptide analog;

X_{11} is any amino acid residue;

X_{12} is any amino acid residue;

X_{13} is a hydrophobic residue;

X_{14} is any amino acid residue;

X_{15} is a hydrophobic residue;

X_{16} is any amino acid residue;

X_{17} is hydrophobic residue or a hydroxyl-substituted aliphatic residue;

Z_{13} is an optional 1 to 5 residue peptide or peptide analog;

Z_{14} is –C(O)OR' or –C(O)NR'R';

each R' is independently hydrogen, (C_1-C_6) alkyl, (C_2-C_6) alkenyl, (C_2-C_6) alkynyl or (C_6-C_{14}) aryl;

each "–" between residues X_{11} through X_{17}, Z_{12} and X_{11} and X_{17} and Z_{13} independently represents an amide linkage, a substituted amide linkage or an isostere of an amide likage; and

each "~" independently represents a bond.

17. The compound of claim 16 wherein said compound further comprises one or more features selected from the group consisting of:

each "–" between residues X_{11} through X_{17}, Z_{12} and X_{11} and X_{17} and Z_{13} is an amide linkage;

Z_{11} is H_2N–;

Z_{14} is –C(O)OH or a salt thereof;

optional Z_{12} is not present;

optional Z_{13} is not present;

X_{11} is other than a basic residue;

X_{13} is an aliphatic residue or M;

X_{14} is other than an aromatic residue;

X_{15} is an aliphatic residue, F or M; and

X_{17} is an aliphatic residue, F, M or a hydroxyl-substituted aliphatic residue.

18. The compound of claim 17 which is selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51 and SEQ ID NO: 52.

19. The compound of claim 16 wherein said compound exhibits antibacterial activity against a Gram-negative bacterium comprising *E. coli, H. influenzae, S. euteriditis, S. typhimurium, B. pertussis, Y. pestis, Y. entarocolitica, H. pylori and K. pneumoniae.*

20. A mannose analogue capable of competitively binding the amino terminal mannose-binding domain of a Gram-negative bacterial adhesin.

21. The analogue of claim 20 wherein said compound exhibits antibacterial activity against a Gram-negative bacterium comprising *Escherichia coli, Haemophilus*

influenzae, Salmonella enteriditis, Salmonella typhimurium, Bordetella pertussis, Yersinia pestis, Yersinia enterocolitica, Helicobacter pylori and Klebsiella pneumoniae.

22. A composition containing an effective amount of a mimic of an amino-terminal motif of a pilus subunit with at least two alternating hydrophobic amino acid residues which mimic exhibits antibacterial activity against a Gram-negative bacterium and a pharmaceutically acceptable carrier, excipient or diluent.

23. The composition of claim 22 wherein said mimic exhibits antibacterial activity by competitively binding to a pilus subunit groove and thereby inhibits pilus assembly.

24. The composition of claim 23 which is a 10 to 20 residue peptide or peptide analog according to formula (I):

(I) Z_1~Z_2–X_1–X_2–X_3–X_4–X_5–X_6–X_7–X_8–X_9–X_{10}–Z_3~Z_4

or a pharmaceutically-acceptable salt thereof, wherein:

Z_1 is R–C(O)–NR– or RRN–;

Z_2 is an optional 1 to 5 residue peptide or peptide analog;

X_1 is any amino acid residue;

X_2 is any amino acid residue;

X_3 is a hydrophobic residue or a hydroxyl-substituted aliphatic residue;

X_4 is any amino acid residue;

X_5 is a hydrophobic residue or Gly;

X_6 is a hydrophobic or a hydrophilic residue;

X_7 is Gly, an amide-substituted polar residue or a hydrophobic residue;

X_8 is any amino acid residue;

X_9 is an aliphatic residue;

X_{10} is any amino acid residue;

Z_3 is an optional 1 to 5 residue peptide or peptide analog;

Z_4 is –C(O)OR or –C(O)NRR;

each R is independently hydrogen, (C_1-C_6) alkyl, (C_2-C_6) alkenyl, (C_2-C_6) alkynyl or (C_6-C_{14}) aryl;

each "–" between residues X_1 through X_{10}, Z_2 and X_1 and X_{10} and Z_3 independently represents an amide linkage, a substituted amide linkage or an isostere of an amide likage and

each "~" represents a bond.

25. The composition of claim 24 wherein the mimic further comprises one or more features selected from the group consisting of:

each "–" between residues X_1 through X_{10}, Z_2 and X_1 and X_{10} and Z_3 is an amide linkage;

Z_1 is H_2N–;

Z_4 is –C(O)OH or a salt thereof;

optional Z_2 is not present;

optional Z_3 is not present;

X_1 is other than a basic residue;

X_2 is other than an aliphatic residue;

X_3 is an aliphatic residue or T;

X_4 is other than an acidic residue;

X_5 is an aliphatic residue, F or G;

X_7 is G, N or A;

X_8 is other than an aliphatic residue; and

X_{10} is an aliphatic or a polar residue.

26. The composition of claim 25 wherein said compound is selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO:

16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

27. A composition containing an effective amount of a mimic of a chaperone G_1 beta-strand with at least two alternating hydrophobic amino acid residues which mimic exhibits antibacterial activity against a Gram-negative bacterium and a pharmaceutically acceptable carrier, excipient or diluent.

28. The composition of claim 27 wherein said mimic exhibits antibacterial activity by competitively binding to a pilus subunit groove and thereby inhibits pilus assembly.

29. The composition of claim 28 which is a 7 to 17 residue peptide or peptide analog according to formula (II):

(II) Z_{11}~Z_{12}–X_{11}–X_{12}–X_{13}–X_{14}–X_{15}–X_{16}–X_{17} –Z_{13}~Z_{14}

or a pharmaceutically-acceptable salt thereof, wherein:

Z_{11} is R'–C(O)–NR'– or R'R'N–;

Z_{12} is an optional 1 to 5 residue peptide or peptide analog;

X_{11} is any amino acid residue;

X_{12} is any amino acid residue;

X_{13} is a hydrophobic residue;

X_{14} is any amino acid residue;

X_{15} is a hydrophobic residue;

X_{16} is any amino acid residue;

X_{17} is hydrophobic residue or a hydroxyl-substituted aliphatic residue;

Z_{13} is an optional 1 to 5 residue peptide or peptide analog;

Z_{14} is –C(O)OR' or –C(O)NR'R';

each R' is independently hydrogen, (C_1-C_6) alkyl, (C_2-C_6) alkenyl,

$(C_2$-$C_6)$ alkynyl or $(C_6$-$C_{14})$ aryl;

each "–" between residues X_{11} through X_{17}, Z_{12} and X_{11} and X_{17} and Z_{13} independently represents an amide linkage, a substituted amide linkage or an isostere of an amide likage; and

each "~" independently represents a bond.

30. The composition of claim 29 wherein said mimic further comprises one or more features selected from the group consisting of:

each "–" between residues X_{11} through X_{17}, Z_{12} and X_{11} and X_{17} and Z_{13} is an amide linkage;

Z_{11} is H_2N–;

Z_{14} is –C(O)OH or a salt thereof;

optional Z_{12} is not present;

optional Z_{13} is not present;

X_{11} is other than a basic residue;

X_{13} is an aliphatic residue or M;

X_{14} is other than an aromatic residue;

X_{15} is an aliphatic residue, F or M; and

X_{17} is an aliphatic residue, F, M or a hydroxyl-substituted aliphatic residue.

31. The composition of claim 30 wherein said mimic is selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51 and SEQ ID NO: 52.

32. The composition of claim 31 wherein the mimic comprises the amino acid sequence NVLQIAL (SEQ ID NO: 1) or an analogue thereof.

33. A composition containing an effective amount of a mannose analogue capable of competitively binding the amino terminal mannose-binding domain of a Gram-negative bacterial adhesin and a pharmaceutically acceptable carrier, excipient or diluent.

34. A method of preventing or inhibiting formation of a pilus subunit-subunit structure in a subject, said method comprising administering a mimic of an N-terminal motif of a pilus subunit with at least two alternating hydrophobic amino acid residues which mimic exhibits antibacterial activity against a Gram-negative bacterium.

35. The method of claim 34 wherein said mimic exhibits antibacterial activity by competitively binding to a pilus subunit groove and thereby inhibits pilus assembly.

36. The method of claim 35 wherein said mimic comprises the amino acid sequence SDVAFRGNLL (SEQ ID NO: 12) or an analogue thereof.

37. The method of claim 36 wherein said subject is a mammal.

38. The method of claim 36 wherein said subject is a plant.

39. A method of preventing or inhibiting formation of a chaperone-subunit structure in a subject, said method comprising administering a mimic of a chaperone G_1 beta strand with least two alternating hydrophobic amino acid residues which mimic exhibits antibacterial activity against a Gram-negative bacterium.

40. The method of claim 39 wherein said mimic exhibits antibacterial activity by competitively binding to a pilus subunit groove and thereby inhibits pilus assembly.

41. The method of claim 40 wherein said mimic comprises the amino acid sequence NVLQIAL (SEQ ID NO: 1) or an analogue thereof.

42. A method of preventing or inhibiting pili adhesion to a host tissue, said method comprising administering a mannose analogue capable of competitively binding the amino terminal mannose-binding domain of a Gram-negative bacterial adhesin.

43. A method of treating a bacterial infection comprising administering to a subject in need thereof an effective amount of a compound which is a 10 to 20 residue peptide or peptide analog according to formula (I):

(I) Z_1~Z_2–X_1–X_2–X_3–X_4–X_5–X_6–X_7–X_8–X_9–X_{10}–Z_3~Z_4

or a pharmaceutically-acceptable salt thereof, wherein:

Z_1 is R–C(O)–NR– or RRN–;

Z_2 is an optional 1 to 5 residue peptide or peptide analog;

X_1 is any amino acid residue;

X_2 is any amino acid residue;

X_3 is a hydrophobic residue or a hydroxyl-substituted aliphatic residue;

X_4 is any amino acid residue;

X_5 is a hydrophobic residue or Gly;

X_6 is a hydrophobic or a hydrophilic residue;

X_7 is Gly, an amide-substituted polar residue or a hydophobic residue;

X_8 is any amino acid residue;

X_9 is an aliphatic residue;

X_{10} is any amino acid residue;

Z_3 is an optional 1 to 5 residue peptide or peptide analog;

Z_4 is –C(O)OR or –C(O)NRR;

each R is independently hydrogen, (C_1-C_6) alkyl, (C_2-C_6) alkenyl, (C_2-C_6) alkynyl or (C_6-C_{14}) aryl;

each "–" between residues X_1 through X_{10}, Z_2 and X_1 and X_{10} and Z_3 independently represents an amide linkage, a substituted amide linkage or an isostere of an amide likage; and

each "~" represents a bond.

44. The method of claim 43 wherein said compound further comprises one or more features selected from the group consisting of:

each "–" between residues X_1 through X_{10}, Z_2 and X_1 and X_{10} and Z_3 is an amide linkage;

Z_1 is H_2N–;

Z_4 is –C(O)OH or a salt thereof;

optional Z_2 is not present;

optional Z_3 is not present;

X_1 is other than a basic residue;

X_2 is other than an aliphatic residue;

X_3 is an aliphatic residue or T;

X_4 is other than an acidic residue;

X_5 is an aliphatic residue, F or G;

X_7 is G, N or A;

X_8 is other than an aliphatic residue; and

X_{10} is an aliphatic or a polar residue.

45. The method of claim 44 wherein said compound is selected from the group consisting SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

46. The method of claim 45 wherein said mimic comprises the amino acid sequence SDVAFRGNLL (SEQ ID NO: 12) or an analogue thereof.

47. The method of claim 42 wherein the infection is caused by E. *coli, H. influenzae, S. euteriditis, S. typhimurium, B. pertussis, Y. pestis, Y. entarocolitica, H. pylori and K. pneumoniae.*

48. The method of claim 42 wherein the subject is a mammal or human.

49. The method of claim 42 wherein the subject is a plant.

50. A method of treating a bacterial infection comprising administering to a subject in need thereof an effective amount of a compound which is a 7 to 17 residue peptide or peptide analog according to formula (II):

(II) Z_{11}~Z_{12}–X_{11}–X_{12}–X_{13}–X_{14}–X_{15}–X_{16}–X_{17}–Z_{13}~Z_{14}

or a pharmaceutically-acceptable salt thereof, wherein:

Z_{11} is R'–C(O)–NR'– or R'R'N–;

Z_{12} is an optional 1 to 5 residue peptide or peptide analog;

X_{11} is any amino acid residue;

X_{12} is any amino acid residue;

X_{13} is a hydrophobic residue;

X_{14} is a hydrophobic or a hydrophilic residue;

X_{15} is a hydrophobic residue;

X_{16} is any amino acid residue;

X_{17} is hydrophobic residue or a hydroxyl-substituted aliphatic residue;

Z_{13} is an optional 1 to 5 residue peptide or peptide analog;

Z_{14} is –C(O)OR' or –C(O)NR'R';

each R' is independently hydrogen, (C_1-C_6) alkyl, (C_2-C_6) alkenyl, (C_2-C_6) alkynyl or (C_6-C_{14}) aryl;

each "–" between residues X_{11} through X_{17}, Z_{12} and X_{11} and X_{17} and Z_{13} independently represents an amide linkage, a substituted amide linkage or an isostere

of an amide likage; and

each "~" independently represents a bond.

51. The method of claim 50 wherein said compound further comprises one or more features selected from the group consisting of:

each "–" between residues X_{11} through X_{17}, Z_{12} and X_{11} and X_{17} and Z_{13} is an amide linkage;

Z_{11} is H_2N–;

Z_{14} is –C(O)OH or a salt thereof;

optional Z_{13} is not present;

optional Z_{14} is not present;

X_{11} is other than a basic residue;

X_{13} is an aliphatic residue or M;

X_{14} is other than an aromatic residue;

X_{15} is an aliphatic residue, F or M; and

X_{17} is an aliphatic residue, F, M or a hydroxyl-substituted aliphatic residue.

52. The method of claim 51 wherein said compound is selected from the group consisting SEQ ID NO: 1, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51 and SEQ ID NO: 52.

53. The method of claim 50 wherein the bacterial infection is caused by E. *coli, H. influenzae, S. euteriditis, S. typhimurium, B. pertussis, Y. pestis, Y. entarocolitica, H. pylori and K. pneumoniae.*

54. The method of claim 50 wherein the subject is a mammal or a human.

55. The method of claim 50 wherein the subject is a plant.

56. A method of preventing or inhibiting biofilm formation, said method comprising administering an effective amount of an isolated compound which bends to a pilus subunit groove to an environment or surface containing Gram-negative bacteria.

57. The method of claim 56, wherein said compound further comprises a mimic of a chaperone G_1 beta strand with at least two alternating hydrophobic amino acid residues which mimic exhibits antibacterial activity against a Gram-negative bacterium.

58. The method of claim 57 wherein the mimic comprises the amino acid sequence NVLQIAL (SEQ ID NO: 1) or an analogue thereof.

59. The method of claim 56, wherein said compound further comprises a mimic of an amino-terminal motif of a pilus subunit with at least two alternating hydrophobic amino acid residues which mimic exhibits antibacterial activity.

60. The method of claim 56, wherein said compound further comprises a mannose analogue capable of competitively binding the amino terminal mannose-binding domain of a Gram-negative bacterial adhesin.

61. A method for inhibiting bacterial colonization by a Gram-negative organism, said method comprising administering an effective amount of an isolated compound which binds to a pilus subunit groove to an environment or surface containing Gram-negative bacteria.

62. The method of claim 61, wherein said compound further comprises a mimic of a chaperone G_1 beta strand with at least two alternating hydrophobic amino acid

residues which mimic exhibits antibacterial activity against a Gram-negative bacterium.

63. The method of claim 61 wherein the mimic comprises the amino acid sequence NVLQIAL (SEQ ID NO: 1) or an analogue thereof.

64. The method of claim 61, wherein said compound further comprises a mimic of an amino-terminal motif of a pilus subunit with at least two alternating hydrophobic amino acid residues which exhibits antibacterial activity against a Gram-negative bacterium.

65. The method of claim 61, wherein said compound further comprises a mannose analogue capable of competitively binding the amino-terminal mannose-binding domain of a Gram-negative bacterial adhesin.

66. A composition comprising a pilus chaperone-subunit co-complex in crystalline form, wherein said co-complex comprises an amino acid sequence of a G_1 beta-strand of a chaperone and an amino acid sequence of an amino-terminal end of a pilus subunit.

67. The composition of claim 66 wherein said amino acid sequence of the G_1 beta-strand of the chaperone is derived from a N101 to L107 amino acid region of the G_1 beta-strand of a chaperone.

68. The composition of claim 67 wherein the amino acid sequence derived from a G_1 beta-strand of a chaperone is SEQ ID NO: 1.

69. The composition of claim 67 wherein the amino acid sequence derived from an amino acid sequence of an amino-terminal end of a pilus subunit is SEQ ID NO: 12.

70. The composition of claim 66 wherein the pilus chaperone-subunit co-complex in crystalline form is a PapD-PapK chaperone-subunit co-complex.

71. The composition of claim 71 wherein the crystal has a space group of $P2_12_12_1$ with unit cell dimensions of a = 62.1 ± 0.2 angstroms, b = 63.6 ± 0.2 angstroms and c = 92.7 ± 0.2 angstroms.

72. The composition of claim 71, wherein said crystal is of diffraction quality.

73. The composition of claim 71, wherein said crystal is a native crystal.

74. The composition of claim 71, wherein said crystal is a heavy-atom derivative crystal.

75. The composition of claim 71, wherein at least one of PapD or PapK of the PapD-PapK chaperone-subunit co-complex is a mutant.

76. The crystal of claim 75, wherein the mutant is a selenomethionine or selenocysteine mutant.

77. The crystal of claim 75, wherein the mutant is a conservative mutant.

78. The crystal of claim 75, wherein the mutant is a truncated or extended mutant.

79. The composition of claim 66, wherein said crystal is produced by a method comprising the steps of:

(a) mixing a volume of a solution comprising the PapD-PapK chaperone-subunit co-complex with a volume of a reservoir solution comprising a precipitant; and

(b) incubating the mixture obtained in step (a) over the reservoir solution in a closed container, under conditions suitable for crystallization until

the crystal forms.

80. A method of crystallizing a PapD-PapK chaperone-subunit co-complex, said method comprising:

(a) mixing a volume of a solution comprising the PapD-PapK chaperone subunit co-complex with a volume of a reservoir solution comprising a precipitant; and

(b) incubating the mixture obtained in step (a) over the reservoir solution in a closed container, under conditions suitable for crystallization until the crystal forms.

81. A method of identifying an antibacterial compound, comprising the step of using a three-dimensional structural representation of a pilus chaperone-subunit co-complex, or a fragment thereof comprising a G_1 beta-strand binding cleft, to computationally screen a candidate compound for an ability to bind the G_1 beta-strand binding cleft of the pilus subunit.

82. The method of claim 81 further comprising the steps of:

synthesizing the candidate compound; and

screening the candidate compound for antibacterial activity.

83. The method of claim 81 wherein the three-dimensional structural information comprises the atomic structure coordinates of a PapK subunit.

84. The method of claim 83 wherein the three-dimensional structural information further comprises the atomic structure coordinates of residues comprising the G_1 beta-strand binding cleft of a PapK subunit.

85. The method of claim 84 wherein the atomic structure coordinates of residues comprising the G_1 beta-strand binding cleft of the PapK subunit are obtained from the atomic structure coordinates of a PapD-PapK chaperone subunit co-complex.

86. The method of claim 85 wherein the PapD-PapK co-complex atomic structure coordinates are those coordinates deposited at the Protein Data Bank under entry code 1PDK.

87. The method of claim 81 wherein the structural information comprises the atomic structure coordinates of a FimH subunit.

88. The method of claim 87 wherein the structural information further comprises the atomic structure coordinates of residues comprising a G_1 beta-strand binding cleft of a FimH subunit.

89. The method of claim 88 wherein the atomic structure coordinates are obtained from the atomic structure coordinates of a FimC-FimH chaperone-adhesin co-complex.

90. The method of claim 89 wherein the atomic structure coordinates are those coordinates deposited at the Research Collaboratory for Structural Bioinformatics Protein Data Bank under entry code 1QUN.

91. A method of identifying an antibacterial compound comprising the step of using a three-dimensional structural representation of a pilus chaperone-subunit co-complex, or a fragment thereof comprising a G_1 beta-strand binding cleft, to computationally design a synthesizable candidate compound that binds the G_1 beta-strand binding cleft of a pilus subunit.

92. The method of claim 91 wherein the computational design comprises the steps of:

identifying chemical entities or fragments capable of associating with the G_1 beta-strand binding cleft of the pilus subunit; and

assembling the chemical entities or fragments into a single molecule to provide the structure of the candidate compound.

93. The method of claim 92 further including the steps of:
synthesizing the candidate compound; and
screening the candidate compound for antibacterial activity.

94. The method of claim 93 wherein the structural information comprises the atomic structure coordinates of a PapK subunit.

95. The method of claim 94 wherein the structural information further comprises the atomic structure coordinates of residues comprising the G_1 beta-strand binding cleft of a PapK subunit.

96. The method of claim 95 wherein the atomic structure coordinates are obtained from the atomic structure coordinates of a PapD-PapK chaperone-subunit co-complex.

97. The method of claim 96 wherein the PapD-PapK co-complex atomic structure coordinates are those coordinates deposited at the Protein Data Bank under entry code 1PDK.

98. The method of claim 93 wherein the structural information comprises the atomic structure coordinates of a FimH subunit.

99. The method of claim 98 wherein the structural information comprises the atomic structure coordinates of residues comprising a G_1 beta-strand binding cleft of a FimH subunit.

100. The method of claim 99 wherein the atomic structure coordinates are obtained from the atomic structure coordinates of a FimC-FimH chaperone-adhesin co-complex.

101. The method of claim 100 wherein the atomic structure coordinates are those

coordinates deposited at the Research Collaboratory for Structural Bioinformatics Protein Data Bank under entry code 1QUN.

102. A method of identifying a compound having antibacterial activity, comprising the step of using a three-dimensional structural representation of a pilus chaperone, or a fragment thereof comprising a G_1 beta-strand, to identify or design a compound having a three-dimensional structure similar to the three-dimensional structure of the G_1 beta-strand of the pilus chaperone.

103. The method of claim 102 wherein the three-dimensional structural information comprises the atomic structure coordinates of residues comprising a G_1 beta-strand of a PapD chaperone or a FimC chaperone.

104. The method of claim 103 wherein the three dimensional structural information comprises the atomic structure coordinates of a PapD chaperone.

105. The method of claim 104 wherein the atomic structure coordinates of the PapD chaperone are obtained from the atomic structure coordinates of a PapD-PapK chaperone-subunit co-complex.

106. The method of claim 105 wherein the atomic structure coordinates of the PapD-PapK chaperone-subunit co-complex are those deposited at the Protein Data Bank under entry code 1PDK.

107. The method of claim 103 wherein the three-dimensional structural information comprises the atomic structure coordinates of a FimC chaperone.

108. The method of claim 107 wherein the atomic structure coordinates of the FimC chaperone are obtained from the atomic structure coordinates of a FimC-FimH chaperone-adhesin co-complex.

109. The method of claim 108 wherein the structure coordinates of the FimC-FimH chaperone-adhesin co-complex are those deposited at the Research Collaboratory for Structural Bioinformatics Protein Data Bank under entry code 1QUN.

110. A method of identifying an antibacterial compound, said method comprising the step of using a three-dimensional structural representation of an adhesin, or a fragment thereof comprising a lectin binding domain, or a portion thereof, to screen a candidate compound for the ability to bind a lectin binding domain of the adhesin.

111. The method of claim 110, further comprising the steps of:

synthesizing the candidate compound; and

assaying the candidate compound for antibacterial activity.

112. The method of claim 111, wherein the three-dimensional structural information comprises the atomic structure coordinates of a FimH adhesin.

113. The method of claim 112 wherein the three-dimensional structural information further comprises the atomic structure coordinates of residues comprising a lectin binding domain of a FimH adhesin or portion thereof.

114. The method of claim 113 wherein the atomic structure coordinates are obtained from the structure coordinates of a FimC-FimH chaperone-adhesin co-complex.

115. The method of claim 114 wherein the structure coordinates of the FimC-FimH chaperone adhesin co-complex are those deposited at the Research Collaboratory for Structural Bioinformatics Protein Data Bank under entry code 1QUN.

116. A method of identifying an antibacterial compound comprising the step of using a three-dimensional structural representation of an adhesin, or a fragment thereof comprising a lectin binding domain or portion thereof, to computationally design a

compound that binds the lectin binding domain of the adhesin.

117. The method of claim 116 wherein the computational design comprises the steps of:

identifying chemical entities or fragments capable of associating with the lectin binding domain; and

assembling the chemical entities or fragments into a single molecule to provide the structure of the candidate compound.

118. The method of claim 117, further comprising the steps of:
synthesizing the candidate compound; and
screening the candidate compound for antibacterial activity.

119. The method of claim 118 wherein the three-dimensional structural information comprises the atomic structure coordinates of a FimH adhesin.

120. The method of claim 119 wherein the three-dimensional structural information further comprises the atomic structure coordinates of residues comprising a lectin binding domain of a FimH adhesin.

121. The method of claim 120 wherein the atomic structure coordinates are obtained from the structure coordinates of a FimC-FimH chaperone-adhesin co-complex or portion thereof.

122. The method of claim 121 wherein the structure coordinates of the FimC-FimH chaperone-adhesin co-complex are those deposited at the Research Collaboratory for Structural Bioinformatics Protein Data Bank under entry code 1QUN.

123. A machine-readable medium embedded with information that corresponds to a three-dimensional structural representation of a crystalline pilus chaperone-subunit co-complex or a fragment or portion thereof.

124. The machine-readable medium of claim 123 wherein the pilus chaperone-subunit co-complex is a PapD-PapK chaperone-subunit co-complex.

125. The machine-readable medium of claim 124 wherein at least one subunit of the PapD-PapK co-complex is a mutant.

126. The machine-readable medium of claim 125 wherein the mutant is a selenomethionine or selenocysteine mutant.

127. The machine-readable medium of claim 125 wherein the mutant is a conservative mutant.

128. The machine-readable medium of claim 124, in which the information comprises atomic structure coordinates, or a subset thereof.

129. The machine-readable medium of claim 128 wherein the atomic structure coordinates are those deposited at the Protein Data Bank under entry code 1PDK, or a subset thereof.

130. The machine-readable medium of claim 123 wherein the pilus chaperone-subunit co-complex is a FimC-FimH chaperone-adhesin co-complex.

131. The machine-readable medium of claim 130 wherein at least one subunit of the FimC-FimH chaperone-adhesin co-complex is a mutant.

132. The machine-readable medium of claim 131 wherein the mutant is a selenomethionine or selenocysteine mutant.

133. The machine-readable medium of claim 131 wherein the mutant is a conservative mutant.

134. The machine-readable medium of claim 130, in which the information comprises atomic structure coordinates, or a subset thereof.

135. The machine-readable medium of claim 134 wherein the atomic structure coordinates are those deposited at the Research Collaboratory for Structural Bioinformatics Protein Data Bank under entry code 1QUN, or a subset thereof.

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